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# SEQUENCE LISTING

<110> KIM, DO-MAN  
KANG, HEE-KYOUNG  
LEE, JIN-HA

<120> PROTEIN WITH ACTIVITY OF HYDROLYZING AMYLOPECTIN, STARCH,  
GLYCOGEN AND AMYLOSE, GENE ENCODING THE SAME, CELL EXPRESSING THE  
SAME, AND PRODUCTION METHOD THEREOF

<130> 44352-0011-00US

<140> 10/588,052

<141> 2006-07-31

<150> PCT/KR05/00235

<151> 2005-01-27

<150> KR 10-2004-0006186

<151> 2004-01-30

<160> 83

<170> PatentIn version 3.3

<210> 1

<211> 647

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
polypeptide

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Val Thr Val Leu Ser Ser Pro Glu Ser Val Thr Ser Ser Asn His Val  
35 40 45

Gln Leu Ala Ser His Glu Met Cys Asp Ser Thr Leu Ser Ala Ser Leu  
50 55 60

Tyr Ile Tyr Asn Asp Asp Tyr Asp Lys Ile Val Thr Leu Tyr Tyr Leu  
65 70 75 80

Thr Ser Ser Gly Thr Thr Gly Ser Val Thr Ala Ser Tyr Ser Ser Ser  
85 90 95

Leu Ser Asn Asn Trp Glu Leu Trp Ser Leu Ser Ala Pro Ala Ala Asp  
 100 105 110

Ala Val Glu Ile Thr Gly Ala Ser Tyr Val Asp Ser Asp Ala Ser Ala  
 115 120 125

Thr Tyr Ala Thr Ser Phe Asp Ile Pro Leu Thr Thr Thr Thr Thr Ser  
 130 135 140

Ser Ser Ser Ala Ser Ala Thr Ser Thr Ser Ser Leu Thr Thr Thr Ser  
 145 150 155 160

Ser Val Ser Ile Ser Val Ser Val Pro Thr Gly Thr Ala Ala Asn Trp  
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Arg Gly Arg Ala Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Thr  
 180 185 190

Asp Gly Ser Thr Thr Tyr Leu Cys Asp Val Thr Asp Arg Val Tyr Cys  
 195 200 205

Gly Gly Ser Tyr Gln Gly Ile Ile Asn Met Leu Asp Tyr Ile Gln Gly  
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Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Ile Val Glu Asn Ile Pro  
 225 230 235 240

Asp Asp Thr Gly Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met Lys Asp  
 245 250 255

Ile Phe Ala Leu Asn Thr Asn Phe Gly Thr Ala Asp Asp Leu Ile Ala  
 260 265 270

Leu Ala Thr Glu Leu His Asn Arg Gly Met Tyr Leu Met Val Asp Ile  
 275 280 285

Val Val Asn His Phe Ala Phe Ser Gly Ser His Ala Asp Val Asp Tyr  
 290 295 300

Ser Glu Tyr Phe Pro Tyr Ser Ser Gln Asp Tyr Phe His Ser Phe Cys  
 305 310 315 320

Trp Ile Thr Asp Tyr Ser Asn Gln Thr Asn Val Glu Gln Cys Trp Leu  
 325 330 335

Gly Asp Asp Thr Val Pro Leu Val Asp Val Asn Thr Gln Leu Asp Thr  
 340 345 350

Val Lys Ser Glu Tyr Gln Ser Trp Val Gln Glu Leu Ile Ala Asn Tyr  
 355 360 365

Ser Ile Asp Gly Leu Arg Ile Asp Thr Val Lys His Val Gln Met Asp  
 370 375 380

Phe Trp Ala Pro Phe Gln Glu Ala Ala Gly Ile Tyr Ala Val Gly Glu  
 385 390 395 400

Val Phe Asp Gly Asp Pro Ser Tyr Thr Cys Pro Tyr Gln Glu Asn Leu  
 405 410 415

Asp Gly Val Leu Asn Tyr Pro Val Tyr Tyr Pro Val Val Ser Ala Phe  
 420 425 430

Glu Ser Val Ser Gly Ser Val Ser Ser Leu Val Asp Met Ile Asp Thr  
 435 440 445

Leu Lys Ser Glu Cys Thr Asp Thr Thr Leu Leu Gly Ser Phe Leu Glu  
 450 455 460

Asn Gln Asp Asn Pro Arg Phe Pro Ser Tyr Thr Ser Asp Glu Ser Leu  
 465 470 475 480

Ile Lys Asn Ala Ile Ala Phe Thr Met Leu Ser Asp Gly Ile Pro Ile  
 485 490 495

Ile Tyr Tyr Gly Gln Glu Gln Gly Leu Asn Gly Gly Asn Asp Pro Tyr  
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Asn Arg Glu Ala Leu Trp Leu Thr Gly Tyr Ser Thr Thr Ser Thr Phe  
 515 520 525

Tyr Lys Tyr Ile Ala Ser Leu Asn Gln Ile Arg Asn Gln Ala Ile Tyr  
 530 535 540

Lys Asp Asp Thr Tyr Leu Thr Tyr Gln Asn Trp Val Ile Tyr Ser Asp  
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Ser Thr Thr Ile Ala Met Arg Lys Gly Phe Thr Gly Asn Gln Ile Ile  
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Thr Val Leu Ser Asn Leu Gly Thr Ser Gly Ser Ser Tyr Thr Leu Thr  
 580 585 590

Leu Ser Asn Thr Gly Tyr Thr Ala Ser Ser Val Val Tyr Glu Ile Leu  
 595 600 605

Thr Cys Thr Ala Val Thr Val Asp Ser Ser Gly Asn Leu Ala Val Pro  
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Ser Pro Ile Val Val Ala Arg Tyr Ile Leu Arg Arg Asp Cys Thr Thr	
20 25 30	
gtt acg gtc ttg tcc tcc cct gag tct gtg acg agt tcg aac cat gtt	144
Val Thr Val Leu Ser Ser Pro Glu Ser Val Thr Ser Ser Asn His Val	
35 40 45	
cag cta gcc agt cat gag atg tgc gac agt acc ttg tca gcg tcc ctt	192
Gln Leu Ala Ser His Glu Met Cys Asp Ser Thr Leu Ser Ala Ser Leu	
50 55 60	

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aca Thr	tcg Ser	tcg Ser	ggc Gly	aca Thr 85	act Thr	ggg Gly	tcc Ser	gta Val	aca Thr 90	gcg Ala	tct Ser	tat Tyr	tct Ser	tct Ser	agt Ser	288
ttg Leu	agt Ser	aac Asn	aac Asn 100	tgg Trp	gaa Glu	ttg Leu	tgg Trp	tct Ser 105	ctc Leu	tcg Ser	gct Ala	ccg Pro	gct Ala 110	gca Ala	gat Asp	336
gct Ala	gtc Val	gag Glu 115	atc Ile	act Thr	gga Gly	gct Ala	agt Ser 120	tat Tyr	gta Val	gac Asp	agc Ser	gat Asp 125	gca Ala	tct Ser	gcg Ala	384
aca Thr 130	tac Tyr	gcc Ala	acg Thr	tct Ser	ttt Phe	gat Asp 135	ata Ile	cct Pro	ctt Leu	act Thr	acc Thr 140	acg Thr	aca Thr	acg Thr	tcg Ser	432
tcg Ser 145	tct Ser	tct Ser	gct Ala	agt Ser	gcg Ala 150	act Thr	tca Ser	aca Thr	tct Ser	agt Ser 155	cta Leu	acc Thr	aca Thr	aca Thr	tct Ser 160	480
agt Ser	gtt Val	tcc Ser	att Ile	tcg Ser 165	gtg Val	tcc Ser	gtc Val	cct Pro	aca Thr 170	gga Gly	aca Thr	gct Ala	gca Ala	aat Asn 175	tgg Trp	528
cga Arg	ggt Gly	agg Arg	gct Ala 180	atc Ile	tat Tyr	cag Gln	atc Ile	gtg Val 185	act Thr	gat Asp	aga Arg	ttt Phe	gca Ala 190	cgc Arg	act Thr	576
gac Asp	ggc Gly	tcc Ser 195	acc Thr	aca Thr	tat Tyr	tta Leu	tgc Cys 200	gat Asp	gtt Val	acc Thr	gat Asp 205	agg Arg	gtc Val	tat Tyr	tgc Cys	624
gga Gly 210	ggg Gly	tct Ser	tat Tyr	cag Gln	ggg Gly	att Ile 215	atc Ile	aat Asn	atg Met	ctg Leu	gat Asp 220	tac Tyr	atc Ile	caa Gln	ggc Gly	672
atg Met 225	ggc Gly	ttt Phe	act Thr	gct Ala	att Ile 230	tgg Trp	att Ile	tct Ser	cct Pro	ata Ile 235	gtg Val	gaa Glu	aat Asn	att Ile	ccc Pro 240	720
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atc Ile	ttc Phe	gcc Ala	ctg Leu 260	aat Asn	aca Thr	aat Asn	ttt Phe	ggt Gly 265	act Thr	gca Ala	gac Asp	gat Asp	ttg Leu 270	ata Ile	gcg Ala	816
ttg Leu	gct Ala	acg Thr 275	gaa Glu	ttg Leu	cat His	aat Asn	cgc Arg 280	ggc Gly	atg Met	tac Tyr	ttg Leu	atg Met 285	gtt Val	gat Asp	att Ile	864

gtt	gtc	aat	cac	ttt	gct	ttc	tca	gga	agt	cat	gcc	gac	gtg	gac	tac	912
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Ser	Glu	Tyr	Phe	Pro	Tyr	Ser	Ser	Gln	Asp	Tyr	Phe	His	Ser	Phe	Cys	
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Trp	Ile	Thr	Asp	Tyr	Ser	Asn	Gln	Thr	Asn	Val	Glu	Gln	Cys	Trp	Leu	
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ggc	gac	gat	act	gtt	cct	ctc	gtg	gac	gtc	aat	acc	caa	ctt	gac	acc	1056
Gly	Asp	Asp	Thr	Val	Pro	Leu	Val	Asp	Val	Asn	Thr	Gln	Leu	Asp	Thr	
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gtg	aaa	agt	gaa	tat	caa	tcc	tgg	gtt	caa	gaa	ctt	ata	gct	aat	tac	1104
Val	Lys	Ser	Glu	Tyr	Gln	Ser	Trp	Val	Gln	Glu	Leu	Ile	Ala	Asn	Tyr	
	355						360					365				
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Ser	Ile	Asp	Gly	Leu	Arg	Ile	Asp	Thr	Val	Lys	His	Val	Gln	Met	Asp	
	370					375					380					
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Phe	Trp	Ala	Pro	Phe	Gln	Glu	Ala	Ala	Gly	Ile	Tyr	Ala	Val	Gly	Glu	
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Val	Phe	Asp	Gly	Asp	Pro	Ser	Tyr	Thr	Cys	Pro	Tyr	Gln	Glu	Asn	Leu	
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gac	ggg	gtc	ttg	aat	tat	cct	gtt	tat	tat	cct	gtc	gtc	tct	gcg	ttt	1296
Asp	Gly	Val	Leu	Asn	Tyr	Pro	Val	Tyr	Tyr	Pro	Val	Val	Ser	Ala	Phe	
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gag	agt	gtt	agt	ggg	tcg	gtc	tcc	tcg	tta	gtc	gat	atg	att	gat	acg	1344
Glu	Ser	Val	Ser	Gly	Ser	Val	Ser	Ser	Leu	Val	Asp	Met	Ile	Asp	Thr	
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ctc	aag	tct	gaa	tgc	acc	gac	act	act	ctc	cta	ggc	tcc	ttt	cta	gag	1392
Leu	Lys	Ser	Glu	Cys	Thr	Asp	Thr	Thr	Leu	Leu	Gly	Ser	Phe	Leu	Glu	
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aat	caa	gat	aat	ccg	cga	ttc	cct	agc	tac	act	tct	gat	gag	tct	tta	1440
Asn	Gln	Asp	Asn	Pro	Arg	Phe	Pro	Ser	Tyr	Thr	Ser	Asp	Glu	Ser	Leu	
465					470					475					480	
att	aaa	aat	gcg	atc	gct	ttc	act	atg	ctc	tca	gac	ggc	att	ccc	ata	1488
Ile	Lys	Asn	Ala	Ile	Ala	Phe	Thr	Met	Leu	Ser	Asp	Gly	Ile	Pro	Ile	
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att	tat	tac	ggg	cag	gag	caa	ggc	ctc	aat	ggg	gga	aac	gat	ccc	tat	1536
Ile	Tyr	Tyr	Gly	Gln	Glu	Gln	Gly	Leu	Asn	Gly	Gly	Asn	Asp	Pro	Tyr	
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Asn Arg Glu Ala Leu Trp Leu Thr Gly Tyr Ser Thr Thr Ser Thr Phe	
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tac aaa tac att gcg tcg ttg aat cag att aga aat cag gct ata tac	1632
Tyr Lys Tyr Ile Ala Ser Leu Asn Gln Ile Arg Asn Gln Ala Ile Tyr	
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aaa gat gat act tat ctc aca tat cag aac tgg gtt att tat tcg gat	1680
Lys Asp Asp Thr Tyr Leu Thr Tyr Gln Asn Trp Val Ile Tyr Ser Asp	
545 550 555 560	
tcc acg aca ata gca atg cgg aaa ggt ttt aca ggg aac caa ata att	1728
Ser Thr Thr Ile Ala Met Arg Lys Gly Phe Thr Gly Asn Gln Ile Ile	
565 570 575	
acg gtt ctg tca aat ctt ggg acc agt ggc agt tcg tac act ttg acg	1776
Thr Val Leu Ser Asn Leu Gly Thr Ser Gly Ser Ser Tyr Thr Leu Thr	
580 585 590	
ctt tcg aat acg gga tat acc gca tct agc gtt gta tat gag atc ttg	1824
Leu Ser Asn Thr Gly Tyr Thr Ala Ser Ser Val Val Tyr Glu Ile Leu	
595 600 605	
aca tgc aca gct gtg act gtg gat tcg tct ggg aat ttg gca gtg ccg	1872
Thr Cys Thr Ala Val Thr Val Asp Ser Ser Gly Asn Leu Ala Val Pro	
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atg tcc agt ggc cta cca aaa gtc ttt tat cag gaa tcg caa ctg gtt	1920
Met Ser Ser Gly Leu Pro Lys Val Phe Tyr Gln Glu Ser Gln Leu Val	
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<210> 40

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<213> Synechococcus sp.

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<213> Zea mays

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